

Fig. 1

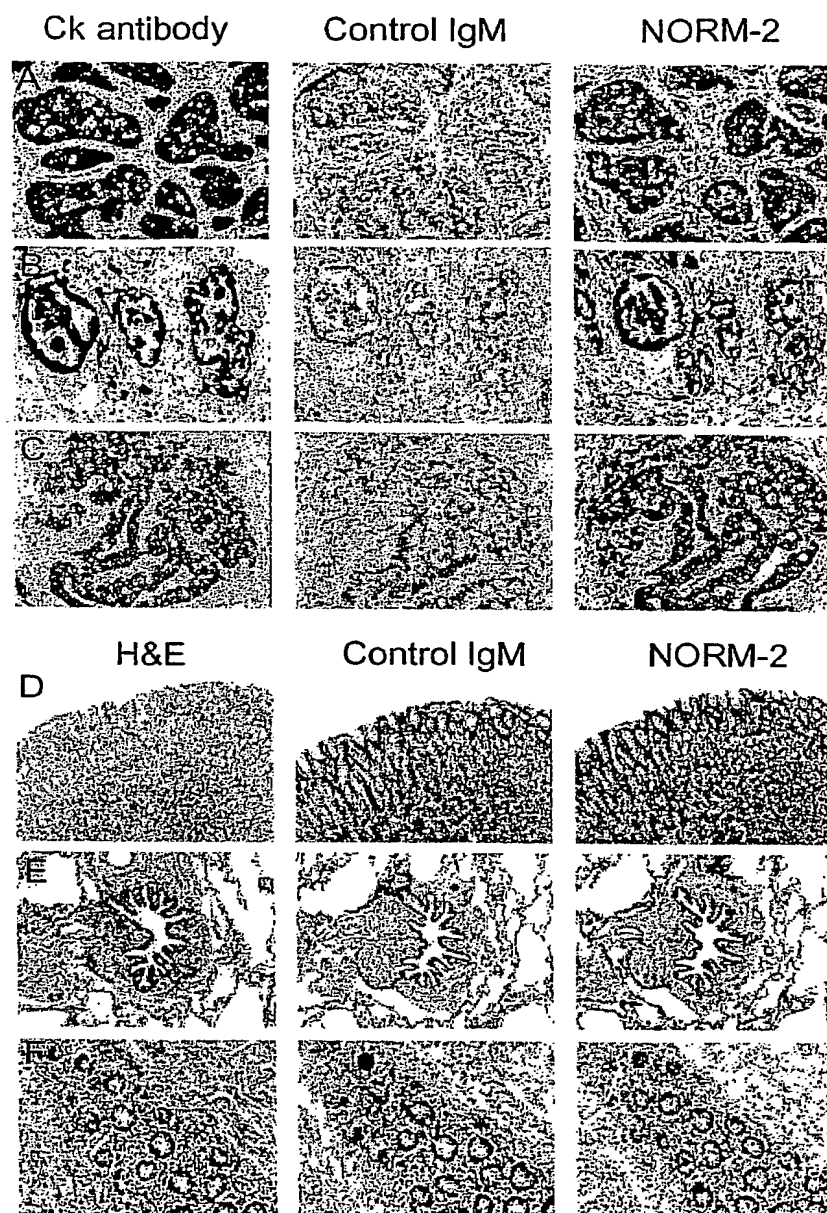


Fig. 2

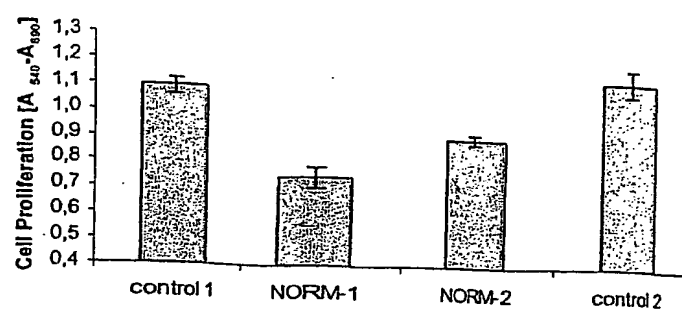


Fig. 3

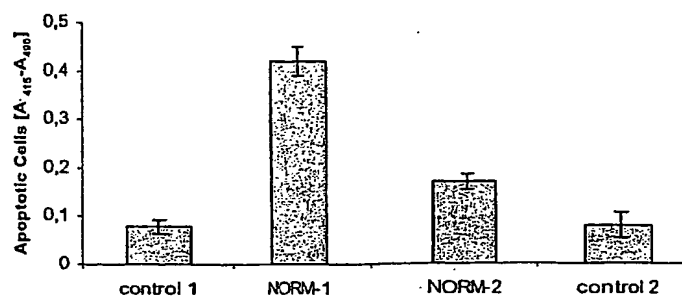


Fig. 4

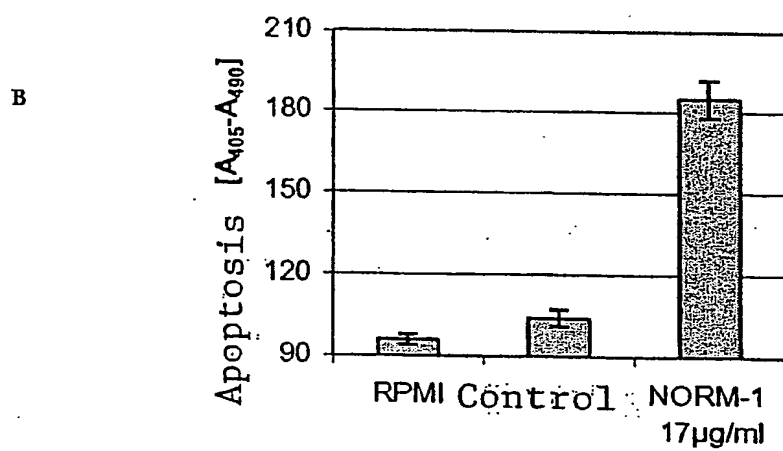
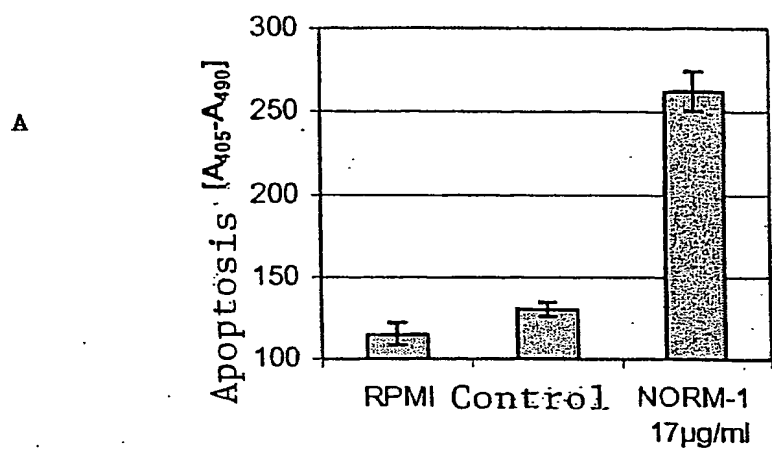


Fig. 5

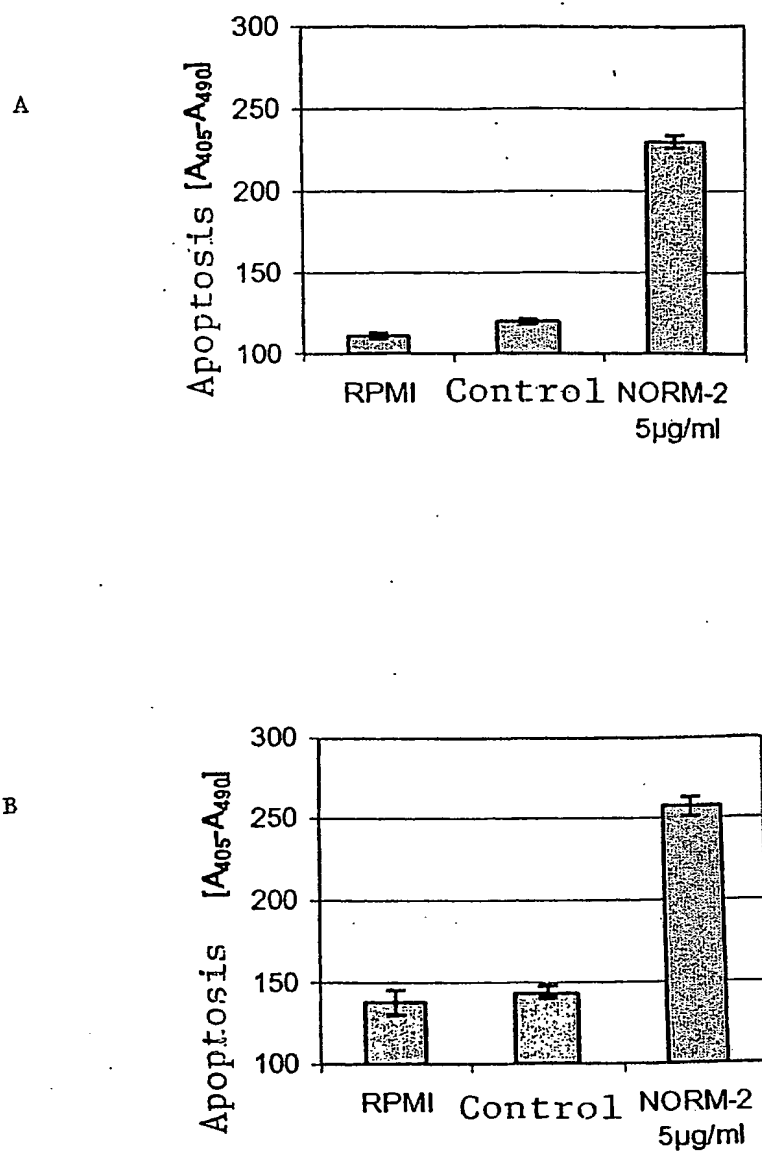


Fig. 6

NORM-1 (VH)

GAG GTG CAG CTG TTG GAG TCT GGG GGA GGC TTG GTA CAG CCT GGG GGG TCC CTG AGA CTC	60
Glu Val Gln Leu Leu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu	20
1 5 10 15 20	
CDR1	
TCC TGT GCA GCC TCT GGA TTC ACC TTT AGC AGC TAT GCC ATG AGC TGG GTC CGC CAG GCT	120
Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala	40
25 30 35 40	
CDR2	
CCA GGG AAG GGG CTG GAG TGG GTC TCA GCT ATT AGT GGT AGT GGT AGC ACA TAC TAC	180
Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr	60
45 50 55 60	
CDR3	
GCA GAC TCC GTG AAG GGC CGG TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT	240
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	80
65 70 75 80	
J-Region	
CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCC GTA TAT TAC TGT GCG AAA GAT GGC	300
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Gly	100
85 90 95 100	
D-Region	
TAT GAT AGT AGT GGT TAT TCG GAA GAA TAT TAC TAC TAC TAC TAC ATG GAC GTC (seq. ID. NO: 2) 357	
Tyr Asp Ser Ser Gly Tyr Ser Glu Glu Tyr Tyr Tyr Tyr Tyr Tyr Met Asp Val (seq. ID. NO: 1)	
105 110 115	

Fig. 7

NORM-1 (VL)

TCC TAT GTG CTG ACT CAG CCA CCC TCG GTG TCA GTG TCC CCA GGA CAA ACG GCC AGG ATC	60
Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Arg Ile	20
1 5 10 15 20	
CDR1	
67 ACC TGC TCT GGA GAT GCA TTG CCA AAA AAA TAT GCT TAT TGG TAC CAG CAG AAG TCA GGC	120
Thr Cys Ser Ser Gly Asp Ala Leu Pro Lys Lys Tyr Ala Tyr Ttp Tyr Gln Gln Lys Ser Gly	40
25 30 35 40	
CDR2	
145 CAG GCC CCT GTG CTG GTC ATC TAT GAG GAC AGC AAA CGA CCC TCC GGG ATC CCT GAG AGA	180
Gln Ala Pro Val Leu Val Ile Tyr Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg	60
45 50 55 60	
CDR3	
262 TTC TCT GGC TCC AGC TCA GGG ACA ATG GCC ACC TTG ACT ATC AGT GGG GCC CAG GTG GAG	240
Phe Ser Gly Ser Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu	80
65 70 75 80	
J-Region	
297 GAT GAA GCT GAC TAC TAC TGT TAC TCA ACA GAC AGC AGT GGT AAT CAT AGC TAT GTG TTC	300
Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Thr Asp Ser Ser Gly Asn His Ser Tyr Val Phe	100
85 90 95 100	

Fig. 8



NORM-2 (VH)

GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC CTG GTC AAG CCT GGG GGG TCC CTG AGA CTC Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu	1 5 10 15 20 60
TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT AGC ATG AAC TGG GTC CGC CAG GCT Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ser Met Asn Trp Val Arg Gln Ala	25 30 35 40 120
CCA GGG AAG GGG CTG GAG TGG GTC TCA TCC ATT AGT AGT AGT AGT TAC ATA TAC TAC Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ser Ser Tyr Ile Tyr Tyr	45 50 55 60 180
GCA GAC TCA GTG AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC TCA CTG TAT Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	65 70 75 80 240
CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCT GTG TAT TAC TGT GCG AGA CAT GGG Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg His Gly	85 90 95 100 300
<div>CDR3</div> <div>J-Region</div> <div>324</div>	
AAC TAC TAC TAC TAC ATG GAC GTC (SEQ. ID. NO: 6)	324
Asn Tyr Tyr Tyr Tyr Met Asp Val (SEQ. ID. NO: 5)	105

Fig. 9

NORM-2 (VL)

CAG TCT GTG TTG ACG CAG CCG CCC TCA GTG TCT GGG GCC CCA GGG CAG AGG GTC ACC ATC	60
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile	20
1 5 10 15 20	
CDR1	
67 TCC TGC ACT GGG AGC AGC TCC AAC ATC GGG GCA GGT TAT GAT GTA CAC TGG TAC CAG CAG	120
Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln	40
25 30 35 40	
CDR2	
154 CTT CCA GGA ACA GCC CCC AAA CTC CTC ATC TAT GGT AAC AGC AAT CGG CCC TCA GGG GTC	180
Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val	60
45 50 55	
CDR3	
271 CCT GAC CCG TTC TCT GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC ACT GGG CTC	240
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu	80
65 70 75 80	
J-Region	
303 CAG GCT GAG GAT GAG GCT GAT TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGT GCC TTG	300
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Ser Ala Leu	100
85 90 95 100	

303  
GTA TTC (seq. ID. NO: 8)  
Val Phe (seq. ID. NO: 7)

Fig. 10

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